Amendments to the Specification

Please replace the paragraph on page 20, lines 12-17, with the following paragraph.

--FIG. 7A shows acridine orange stained spreads visualized with a fluorescent light source. Intact/viable RNA ~~appears orange and DNA green using this procedure and~~ can be readily identified using this procedure. Three stained cells with good quality of RNA are indicated by arrows. FIG. 7B is an IHC on human post mortem brain spread using anti NF--H to identify neurons. Two intact NF--H positive neurons are indicated by arrows. Scale bars are 10 μm.--

Please replace the paragraph on page 25, lines 12-23, with the following paragraph.

--To ensure that the cDNA fragments chosen will yield riboprobes specific only to the message of interest, a full homology search is performed for each potential message of interest. The names of the selected genes are searched in the NCBI database which is maintained by the National Institute of Health (NIH) (~~http://www.ncbi.nlm.nih.gov/dbEST- /index.html~~ www.ncbi.nlm.nih.gov/dbEST- /index.html). This database is a compilation of all; known genes, their sequences, their discoverer, their sequencing orientation and other relevant information. Each entry is given a Genbank accession number which is used for identification purposes. This accession number is also used by various computer programs which link to the NCBI database for analysis of the DNA sequences, amino acid sequences, protein translations, and numerous other tasks. Versa Term PRO and Mac Vector, two programs which link to the NCBI database, were used to generate the information in Table 1. --

Please replace the paragraph bridging pages 37 and 38 with the following paragraph.

--cDNA clones: cDNA clones were identified in the NCBI database of expressed sequence tag libraries (~~http://www.ncbi.nlm.nih.gov/dbEST/index- .html~~ www.ncbi.nlm.nih.gov/dbEST/index- .html) using the Genbank accession numbers of the genes. Only those EST clones isolated from exclusively oligo-dT primed libraries were considered. Homology and position of the EST clones were checked against the original sequence of the genes of interest. EST clones were ordered from the companies which held them (ATCC,

Genome Systems, Inc., or Research Genetics, Inc.). One microgram of each linearized cDNA was denatured with the addition of 1/10 volume 1 M NaOH and incubated at room temperate for 15 minutes. The sample volume was increased to 100 .mu.l with 10.times.SSC and the cDNAs of interest were immediately applied to a 96 well format dot blot apparatus (Gibco/BRL) containing a prewetted nylon membrane (MSI). --